

INFORMATION DISCLOSURE STATEMENT	Atty. Docket No.: 00032.US1	Serial No.: 09/825,212
	Applicant(s): Timothy E. Benson	Confirmation No.: 2707
	Filing Date: April 3, 2001	Group: 1645

U.S. PATENT DOCUMENTS

Examiner Initial	Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
	none					

FOREIGN PATENT DOCUMENTS

Examiner Initial	Document Number	Date	Country	Class	Subclass	Translation	
						Yes	No
NE	EP 786 519 A2	07/30/97	Europe				
NE	WO 99/47639 A2	09/23/99	PCT				
NE	WO 99/47662 A1	09/23/99	PCT				
NE	WO 00/12678 A2	03/09/00	PCT				
NE	WO 00/12678 A3	03/09/00	PCT				
NE	WO 01/16292 A2	03/08/01	PCT				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial	Document Description
NE	Åslund et al., "The thioredoxin superfamily: redundancy, specificity, and gray-area genomics," <i>J Bacteriol.</i> 1999 Mar;181(5):1375-9.
NE	Bartlett et al., "CAVEAT: A program to facilitate the structure-derived design of biologically active molecules," <i>Molecular Recognition: Chemical and Biological Problems</i> , Royal Society of Chemistry, Special Pub No. 78:182-196 (1989).
NE	Benson et al., "An enzyme-substrate complex involved in bacterial cell wall biosynthesis," <i>Nat Struct Biol.</i> 1995 Aug;2(8):644-53.
NE	Blundell et al., <i>Protein Crystallography</i> , Academic Press, New York, NY; title page, publication page, and table of contents only, 8 pages (1976)
NE	Böhm, "The computer program LUDI: a new method for the de novo design of enzyme inhibitors," <i>J Comput Aided Mol Des.</i> 1992 Feb;6(1):61-78.
NE	Brünger, "X-PLOR: Version 3.1, a System for X-Ray Crystallography and NMR", Yale University Press, New Haven & London, 1992; cover page, publication page and table of contents: 13 pages.
NE	Collaborative Computational Project, No. 4, "The CCP4 suite: programs for protein crystallography" <i>Acta Cryst.</i> 1994;D50:760-3.

EXAMINER	<i>Noted 10/12/04</i>	Date Considered
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NE	Cowan et al., "Improvement of Macromolecular Electron-Density Maps by the Simultaneous Application of Real and Reciprocal Space Constraints," <i>Acta Crystallogr D Biol Crystallogr</i> . 1993 Jan 1;49(1):148-157.
NE	Cowan et al., "Miscellaneous algorithms for density modification," <i>Acta Crystallogr D Biol Crystallogr</i> . 1998 Jul 1;54(4):487-93.
NE	Dai et al., "Crystal structure of <i>Arabidopsis thaliana</i> NADPH dependent thioredoxin reductase at 2.5 Å resolution," <i>J Mol Biol</i> . 1996 Dec 20;264(5):1044-57.
NE	delCardayre et al., "Coenzyme A disulfide reductase, the primary low molecular weight disulfide reductase from <i>Staphylococcus aureus</i> . Purification and characterization of the native enzyme," <i>J Biol Chem</i> . 1998 Mar 6;273(10):5744-51.
NE	Eisen et al., "HOOK: a program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," <i>Proteins: Struct. Funct. Genet</i> . 1994 Jul;19(3):199-221.
NE	Evans, "SETOR: hardware-lighted three-dimensional solid model representations of macromolecules," <i>J Mol Graph</i> . 1993 Jun;11(2):134-8.
NE	Finzel, "LORE: exploiting database of known structures," <i>Meth. Enzymol</i> . 1997; 277(B):230-42.
NE	Gillet et al., "SPROUT: a program for structure generation," <i>J Comput Aided Mol Des</i> . 1993 Apr;7(2):127-53.
NE	Goodford, "A computational procedure for determining energetically favorable binding sites on biologically important macromolecules," <i>J Med Chem</i> . 1985 Jul; 28(7):849-57.
NE	Goodsell et al., "Automated docking of substrates to proteins by simulated annealing," <i>Proteins: Struct. Funct. Genet</i> . 1990;8(3):195-202.
NE	Hendrickson, "Determination of macromolecular structures from anomalous diffraction of synchrotron radiation," <i>Science</i> . 1991 Oct 4;254(5028):51-8.
NE	Jiang et al., "Protein hydration observed by X-ray diffraction. Solvation properties of penicillopepsin and neuraminidase crystal structures," <i>J Mol Biol</i> . 1994 Oct 14;243(1):100-15.
NE	Kraulis, "MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures," <i>J. Appl. Cryst</i> . 1991 Oct;24:946-950.

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NE	Kuntz et al., "A geometric approach to macromolecule-ligand interactions," <i>J Mol Biol.</i> 1982 Oct 25;161(2):269-88.
NE	Kuriyan et al., "Crystallization and preliminary x-ray characterization of thioredoxin reductase from <i>Escherichia coli</i> ," <i>J Biol Chem.</i> 1989 Aug 5;264(22):12752-3.
NE	Kuriyan et al., "Convergent evolution of similar function in two structurally divergent enzymes," <i>Nature.</i> 1991 Jul 11;352(6331):172-4.
NE	Laskowski, et al., "PROCHECK: a program to check the stereochemical quality of protein structures," <i>J. Appl Cryst.</i> 1993 Apr;26:283-291
NE	Lattman, "Use of the rotation and translation functions," <i>Methods Enzymol.</i> 1985;115:55-77.
NE	Lauri et al., "CAVEAT: a program to facilitate the design of organic molecules," <i>J Comput Aided Mol Des.</i> 1994 Feb;8(1):51-66.
NE	Lennon et al., "Crystal structure of reduced thioredoxin reductase from <i>Escherichia coli</i> : structural flexibility in the isoalloxazine ring of the flavin adenine dinucleotide cofactor," <i>Protein Sci.</i> 1999 Nov;8(11):2366-79.
NE	Martin, "3D database searching in drug design," <i>J Med Chem.</i> 1992 Jun 12;35(12):2145-54.
NE	Meng et al., "Automated docking with grid-based energy evaluation," <i>J. Comp. Chem.</i> 1992 May;13(4):505-524.
NE	Merritt et al., "Raster3D Version 2.0. A program for photorealistic molecular graphics," <i>Acta Crystallogr D Biol Crystallogr.</i> 1994 Nov;50(6):869-73.
NE	Miranker et al., "Functionality maps of binding sites: a multiple copy simultaneous search method," <i>Proteins: Struct. Funct. Genet.</i> 1991;11(1):29-34.
NE	National Institutes of Health, "BLAST 2 Sequences," [online] United States; retrieved August 29, 2001 from the Internet: http:// www.ncbi.nlm.nih.gov/gorf/bl2.html 1 pg.
NE	Nishibata et al., "Automatic creation of drug candidate structures based on receptor structure. Starting point for artificial lead generation," <i>Tetrahedron</i> , 1991;47(43):8985-90.

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NE	Otwinowski, "Maximum likelihood refinement of Heavy atom parameters," <i>Isomorphous replacement and anomalous scattering - Proceedings of the CCP4 Study Weekend 25-26 January 1991</i> , (W. Wolf et al., eds.) Science and Engineering Research Counsel, Daresbury Laboratory, Warrington, U.K. (1991) pp. 80-86.
NE	Ramakrishnan et al., "Crystal structure of globular domain of histone H5 and its implications for nucleosome binding," <i>Nature</i> . 1993 Mar 18;362(6417):219-23.
NE	Rossmann, ed., <i>The Molecular Replacement Method - A Collection of Papers on the Use of Non-Crystallographic Symmetry</i> , Intl. Sci. Rev. Ser. No. 13, Gordon & Breach, New York, NY; title page, publication page, and table of contents only, 6 pages (1972).
NE	Sack, "CHAIN - A Crystallographic Modeling Program," <i>J Molecular Graphics</i> . 1988 Dec; 6(4):224-5.
NE	Sheldrick et al., "Structure solution by iterative peaklist optimization and tangent expansion in space group P1," <i>Acta Crystallogr B</i> . 1995 Aug 1;51(Pt 4):423-31.
NE	Tatusova et al., "BLAST 2 Sequences, a new tool for comparing protein and nucleotide sequences," <i>FEMS Microbiol Lett</i> . 1999 May 15;174(2):247-50.
NE	Travis, "Proteins and organic solvents make an eye-opening mix," <i>Science</i> . 1993 Nov 26;262(5138):1374.
NE	Van Duyne et al., "Atomic structures of the human immunophilin FKBP-12 complexes with FK506 and rapamycin," <i>J Mol Biol</i> . 1993 Jan 5;229(1):105-24.
NE	Waksman et al., "Crystal structure of <i>Escherichia coli</i> thioredoxin reductase refined at 2 Å resolution. Implications for a large conformational change during catalysis," <i>J Mol Biol</i> . 1994 Feb 25;236(3):800-16.
NE	Williams, "Mechanism and structure of thioredoxin reductase from <i>Escherichia coli</i> ," <i>FASEB J</i> . 1995 Oct;9(13):1267-76.
NE	Wyckoff et al., eds., <i>Methods in Enzymology Vol. 114 - Diffraction Methods for Biological Macromolecules</i> , Academic Press, Orlando, FL; title page, publication page, and table of contents only, 5 pages (1985).
NE	Wyckoff et al., eds., <i>Methods in Enzymology Vol. 115 - Diffraction Methods for Biological Macromolecules</i> , Academic Press, Orlando, FL; title page, publication page, and table of contents only, 4 pages (1985).

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